

296514US0PCT.ST25.txt
SEQUENCE LISTING

<110> Okamoto, Kiyoshi
Kawamura, Takanori
Asano, Makoto
Shitakubo, Daiya
Shirato, Manabu
Asada, Makoto

<120> Using non-human animal model, method of measuring transcription activity, method of measuring cell quantity and method of measuring tumor volume.

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<141> 2006-09-22

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<151> 2005-03-23

<150> Japan 2004-084810
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 Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
 260 265 270
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 Gly Ile Ile Pro Val Glu Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu
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 gca gcc gag gcc ctg ggt gcc gcc aag aag ctg cag cct gca cag aca 144
 Ala Ala Glu Ala Leu Gly Ala Lys Lys Leu Gln Pro Ala Gln Thr
 35 40
 gcc gcc aag aac ctc atc atc ttc ctg ggc gat ggg atg ggg gtg tct 192
 Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
 50 55 60
 acg gtg aca gct gcc agg atc cta aaa ggg cag aag aag gac aaa ctg 240
 Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
 65 70 75
 ggg cct gag ata ccc ctg gcc atg gac cgc ttc cca tat gtg gct ctg 288
 Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
 85 90 95
 tcc aag aca tac aat gta gac aaa cat gtg cca gac agt gga gcc aca 336
 Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
 100 105 110
 gcc acg gcc tac ctg tgc ggg gtc aag ggc aac ttc cag acc att ggc 384
 Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
 115 120 125
 ttg agt gca gcc gcc cgc ttt aac cag tgc aac acg aca cgc ggc aac 432
 Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
 130 135 140
 gag gtc atc tcc gtg atg aat cgg gcc aag aaa gca ggg aag tca gtg 480
 Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
 145 150 155 160
 gga gtg gta acc acc aca cga gtg cag cac gcc tcg cca gcc ggc acc 528
 Gly Val Val Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
 165 170 175
 tac gcc cac acg gtg aac cgc aac tgg tac tcg gac gcc gac gtg cct 576
 Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
 180 185 190
 gcc tcg gcc cgc cag gag ggg tgc cag gac atc gct acg cag ctc atc 624
 Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr 205
 195 200 205
 tcc aac atg gac att gac gtg atc cta ggt gga ggc cga aag tac atg 672
 Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Lys Tyr Met
 210 215 220 225
 ttt cgc atg gga acc cca gac cct gag tac cca gat gac tac agc caa 720
 Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
 225 230 235 240
 ggt ggg acc agg ctg gac ggg aag aat ctg gtg cag gaa tgg ctg gcg 768
 Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
 245 250 255 260

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gcc Gly	ggc Gly	acc Gly	acc Gly	gac Gly	gcc Gly	gcg Gly	cac Gly	ccg Gly	ggt Gly	tac Gly	tct Gly	aga Gly	gtc Gly	ggg Gly	gcg Gly		1536		

Ala Gly Thr Thr Asp Ala Ala His Pro Gly Tyr Ser Arg Val Gly Ala
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1560

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Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr
 35 40 45

Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
 50 55 60

Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
 65 70 75 80

Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
 85 90 95

Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
 100 105 110

Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
 115 120 125

Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
 130 135 140

Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
 145 150 155 160

Gly Val Val Thr Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
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Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
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Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile
195 200

Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Lys Tyr Met
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Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
225 230 235 240

Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
245 250 255

Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
260 265 270

Ala Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro
275 280 285

Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser
290 295 300

Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro
305 310 315 320

Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His
325 330 335

His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp
340 345 350

Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu
355 360 365

Ser Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr
370 375 380

Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg
385 390 395 400

Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr
405 410 415

Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly
420 425 430

Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro Leu Asp Glu Glu Thr
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His Ala Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His
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Leu Val His Gly Val Gln Glu Gln Thr Phe Ile Ala His Val Met Ala
465 470 475 480

Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Pro
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Ala Gly Arg Phe Glu Gln Thr
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22

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33